

FIG. 1

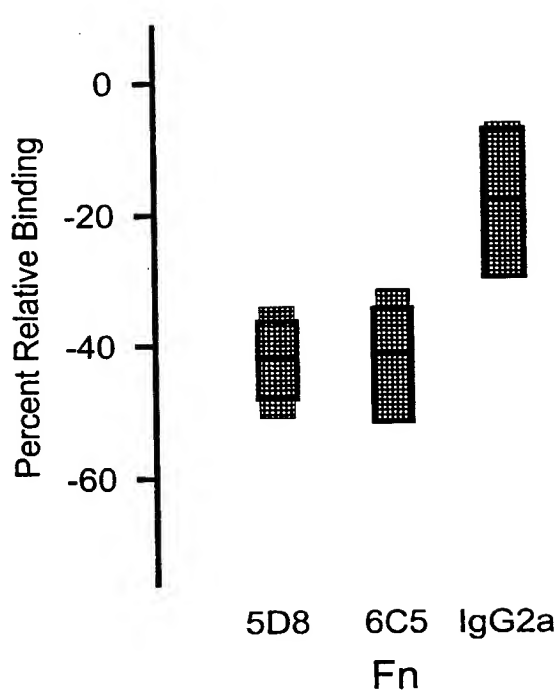


FIG. 2A

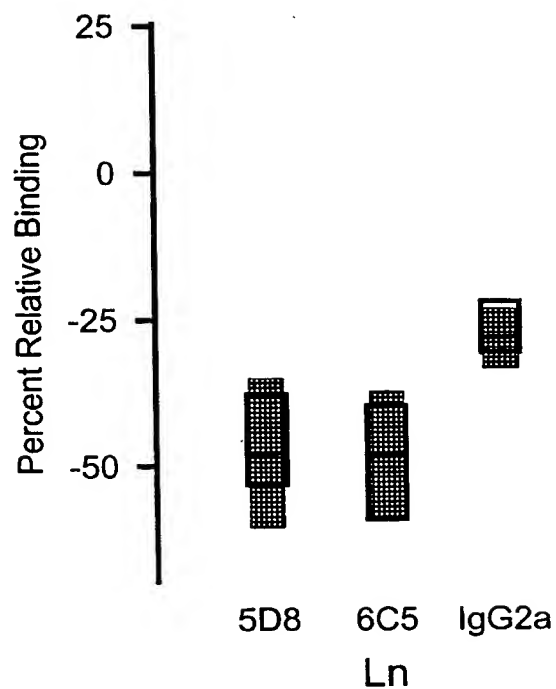


FIG. 2B

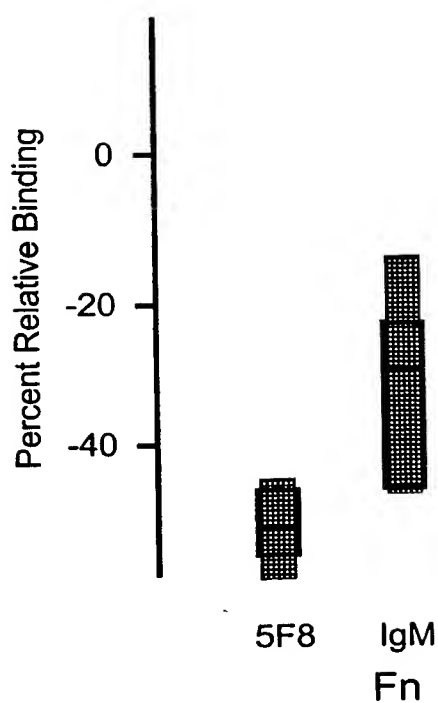


FIG. 2C

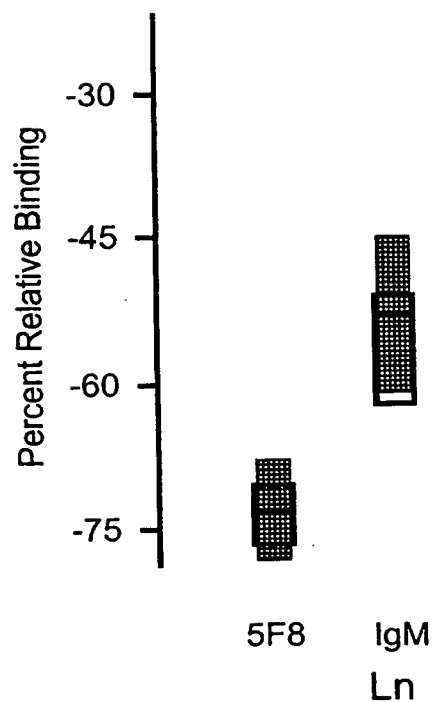


FIG. 2D

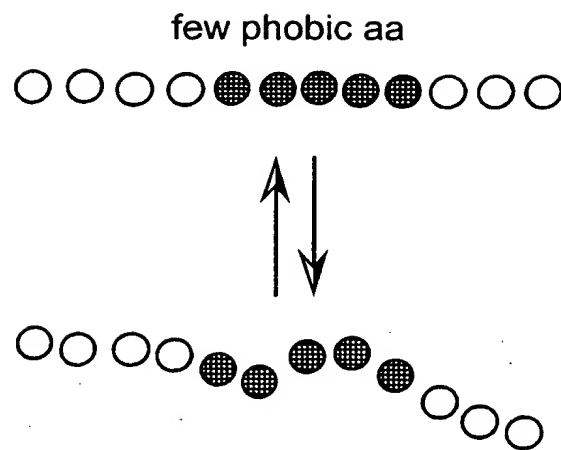


FIG. 3A

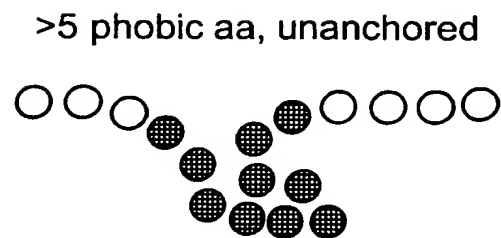


FIG. 3B

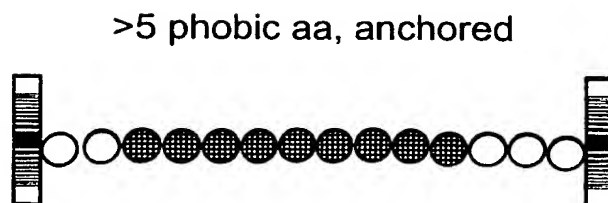


FIG. 3C

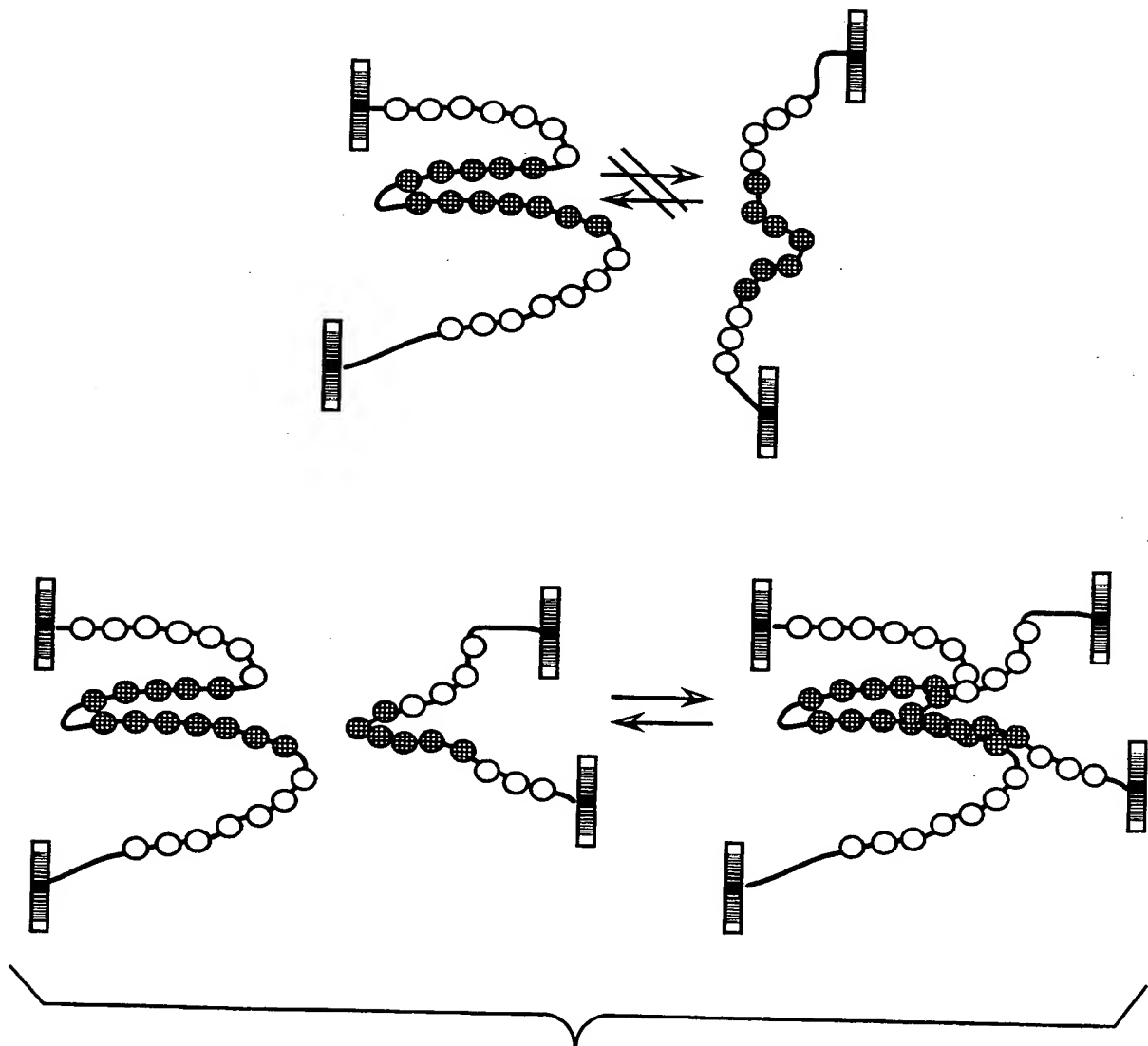


FIG. 4

1 TTTTACCGAACTTGCTAACCTCCCTTATCCCTTTCAAGGAGATTATAAATAGAGATGAAA 60
61 AATCTCTCATCAATTGAAGGATAGTTCCAAATTTATCATTAAAAACAAC TACAATAAC 120
121 TACAACTTAACTTTAACTAAAAAAAAAAACATGTCAATCGATAAATCAAGAATGGTCACC 180
M S I D K S R M V T -
181 AGATTAGGTAAATCTGGTTTGAAGGTCAACACTGTTGCTGTCGGTACTATGAGATTGGGA 240
R L G K S G L K V N T V A V G T M R L G -
241 TCCAGTTGGAGAGGTTTTAATGGTGACATCGACGAGTGTTTGAAAATTTTGAAATTTTGT 300
S S W R G F N G D I D E C L K I L K F C -
301 TATGACAACGGGTTCCGTACTTTGATACTGCTGATACTTACTCAAATGGTAAATCTGAA 360
Y D N G F R T F D T A D T Y S N G K S E -
361 GAGTTGTTGGGTTTATTCATCAAGAAATACAATATTCCACGTGAACGAATTGTCATTTTA 420
E L L G L F I K K Y N I P R E R I V I L -
421 ACCAAATGCTACTTCTCAGTCAAAGACGACGCAGAAGACAGTTCACTTGAAATTGATCCA 480
T K C Y F S V K D D A E D S S L E I D P -
481 ATTGACTATATGAACGGTAAAGGATTGAGCAGAAAGCATATCTTAGCCGCAGCTGAAGCT 540
I D Y M N G K G L S R K H I L A A A E A -
541 TCCGTTAAACGTTTGGGAACATATATTGATGTGTTGCAAATTCATCGTTTAGACCATGAA 600
S V K R L G T Y I D V L Q I H R L D H E -
601 GTCACATATGAAGAGGTTATGCGTTCTTTAAATGATGTTGTTGAACAAGGATTGGCAAGA 660
V T Y E E V M R S L N D V V E Q G L A R -
661 TACATTGGTGCCTCATCTATGAAAACATGGGAATTTGTTGAGTTGCAAAATGTTGCTAAA 720
Y I G A S S M K T W E F V E L Q N V A K -
721 GCAAATGGTTGGCACCAATTCATCTCCATGCAAAGTCACTATTCTTTATTGTACCGTGAG 780
A N G W H Q F I S M Q S H Y S L L Y R E -
781 GACGAGAGAGAATTGAATGACTATTGTAAGAAGAATGGTATTGGATTAATCCCTTGGTCT 840
D E R E L N D Y C K K N G I G L I P W S -

FIGURE 5A

841 CCAAACGGTGGTGGTGTGTTTTGTGTCGTCATTGACTCTGAAAAAACTAAGCAGTTCTTA 900
P N G G G V L C R P F D S E K T K Q F L -

901 GACAACAAGCAATGGTCAAGTTTATTTGGATTAGAAAATGTCAGAGACGCAGATAAGATT 960
D N K Q W S S L F G L E N V R D A D K I -

961 ATCGTCGATAGAGTTGAAGAGTTGAGTGTAAATACAATGCATCTATGATGCAAGTTTCA 1020
I V D R V E E L S V K Y N A S M M Q V S -

1021 TTGGCATGGTGTATTGCTAAAGGTGTGATTCCAATTGCCGGTGTCTCCAAATTTGAGCAA 1080
L A W C I A K G V I P I A G V S K F E Q -

1081 GCTGAAGAATTGGTTGGTATTTTCAAAGTCAACTTAACTGAAGATGATATCAAATATCTT 1140
A E E L V G I F K V N L T E D D I K Y L -

1141 GAAGAGCCATATCACGCCAAAGACTTGGCAAGAGTTGCTGCTTAAGTTTGTATGTAGTT 1200
E E P Y H A K D L A R V A A

1201 TAGCTTTGCTAATCGTTTATCTTTATTAGGTCTAGATATGAATTACAAAATACATGTGTA-1260

1261 TCTTGCCATTTTATATACAAATAAGATTTATCTTGGCTTAA 1301

FIGURE 5B